Draft Genome Sequence of *Burkholderia* sp. Strain MP-1, a Methyl Parathion (MP)-Degrading Bacterium from MP-Contaminated Soil

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Burkholderia sp. strain MP-1 was isolated from pesticide-contaminated soil. Herein, we report the draft genome sequence of strain MP-1, which contains 168 contigs of 8,611,053 bp, with a G+C content of 62.55% and 7,631 protein-coding genes.

*B*urkholderia spp. are widely distributed in nature and include a large variety of related environmental, clinical, and agribiotechnological species (1). The genus *Burkholderia* now comprises 78 species (http://www.bacterio.net/burkholderia.html). A methyl parathion (MP)-degrading bacterial strain, designated as *Burkholderia* sp. strain MP-1 (LMG 27927 = MCCC 1K00250), was isolated from the contaminated soil of a former pesticide-manufacturing company in Jiangsu province of China. The 16S rRNA sequence of the newly isolated strain showed the highest similarity to that of *Burkholderia grimmiae* DSM 25160^T (98.45%) (2).

The genome sequence of strain MP-1 was determined by Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China), with a MiSeq system using paired-end sequencing technology. A total of 3,758,646 pair reads and 9,573 clean single reads (500-bp library; read length, 300 bp $\times$ 2) were assembled using Newbler 2.6. The genome of *Burkholderia* sp. MP-1 contains 168 contigs (>500 bp; N_{90}, 69) of 8,611,053 bp (131-fold coverage), with an average G+C content of 62.55%. Automatic gene annotation was performed by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html). The genome comprises 7,791 genes, including 55 tRNA genes for all 20 amino acids, 3 rRNA genes, 1 small noncoding RNA gene, 101 pseudogenes, and 7,631 protein-coding genes (CDS) (with an average length of 950 bp), which give a coding intensity of 84.2%. In all, 4,853 proteins were assigned to Clusters of Orthologous Groups (COG) families (3). Among these proteins, the ones associated with general function prediction (R; 860 open reading frames [ORFs], 17.7%) are the most abundant content of COG, followed by the proteins related to amino acid transport and metabolism (E; 744 ORFs, 15.3%) and transcription (K; 534 ORFs, 11.0%).

Strain MP-1 was able to metabolize MP, a common organophosphorus pesticide employed as the sole carbon source for growth. According to the annotation results, the gene encoding phosphotriesterase exists in the genome. Several draft genomes of *Burkholderia* strains were investigated, such as that of *Burkholderia pyrrocinia* CH-67, whose genome contains genes encoding enzymes for aromatic compound degradation (4). The genome sequence of strain MP-1 and its curated annotation were analyzed to provide abundant genetic information and to explore useful functions.

Nucleotide sequence accession number. The draft genome sequence of strain MP-1 has been deposited at GenBank under the accession no. JFHF00000000 (chromosome).

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